

HN #4



PCT09

ENTERED

## RAW SEQUENCE LISTING

DATE: 03/28/2002

PATENT APPLICATION: US/09/936,377

TIME: 10:55:51

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\03282002\I936377.raw

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4 <110> APPLICANT: DeFrenne, Catherine
5      DelMelle, Christine
6      Ruelle, Jean-Louis
8 <120> TITLE OF INVENTION: Novel Compounds
11 <130> FILE REFERENCE: BM45379
13 <140> CURRENT APPLICATION NUMBER: 09/936,377
C--> 14 <141> CURRENT FILING DATE: 2002-02-26
16 <150> PRIOR APPLICATION NUMBER: 9905815.8
17 <151> PRIOR FILING DATE: 1999-03-12
19 <150> PRIOR APPLICATION NUMBER: 9909094.6
20 <151> PRIOR FILING DATE: 1999-04-21
22 <150> PRIOR APPLICATION NUMBER: 9909503.6
23 <151> PRIOR FILING DATE: 1999-04-23
25 <150> PRIOR APPLICATION NUMBER: 9909787.5
26 <151> PRIOR FILING DATE: 1999-04-28
28 <150> PRIOR APPLICATION NUMBER: 9910710.4
29 <151> PRIOR FILING DATE: 1999-05-07
31 <150> PRIOR APPLICATION NUMBER: PCT/EP00/09155
32 <151> PRIOR FILING DATE: 2000-03-07
34 <160> NUMBER OF SEQ ID NOS: 10
36 <170> SOFTWARE: FastSEQ for Windows Version 4.0
38 <210> SEQ ID NO: 1
39 <211> LENGTH: 2277
40 <212> TYPE: DNA
41 <213> ORGANISM: Neisseria meningitidis
43 <400> SEQUENCE: 1
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46 aaaagccgtc cgcgcgccac atcagggctg ctgcacactt cgaccgcctc cgacaaaatc      180
47 atcagcggcg acaccttgcg acaaaaagcc gtcaacttgg gcgatgcttt ggacggcgtg      240
48 ccggggcattc acgcctcgca atacggcggc ggcgcgtccg ctcccgttat tcgcggtcaa      300
49 acaggcagac ggattaaagt attgaacct caaggcgaaa caggcgatat ggcggtattt      360
50 tcgcccgatc acgccattat ggtagatacc gccttgtcgc aacaggtcga aatcctgcgc      420
51 gggcccggtta cgtctttgta cagctcgggc aatgtggcgg ggctggtcga tgttgccgat      480
52 ggcaaaaatcc ccgaaaaaat gcctgaaaac ggcgtatcgg gcgaactcgg attgcgtttg      540
53 agcagcggca atctggaaaa actcacgtcc ggcggcatca atatcggttt gggcaaaaac      600
54 tttgtattgc acacggaagg gctgtaccgc aaatcggggg attacgccgt accgcgttac      660
55 cgcaatctga aacgcctgcc cgacagccca cgccgattcg caaacgggca gcatcgggct      720
56 gtcttggggtt ggcgaaaaag gttttatcgg cgtacgtaca gcgaccgtcg cgaccaatat      780
57 ggtctgcctg cccacagcca cgaatacga gattgccacg ccgacatcat ctggcaaaag      840
58 agcttgatta acaaacgcta ttacagctt taccgcacc tgttgaccga agaagacgtc      900
59 gattacgaca atccgggctt gagctgcggc ttccacgacg acgatgatgc acacgcccac      960
60 gcccaaacg gcaaaccttg gatagacctg cgcaacaaac gctacgaact ccgcgccgaa      1020

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61  tggaagcagc  cattccccgg  ttttgaagcc  ctgcgcgtac  acctgaaccg  caacgactac  1080
62  caccacgacg  aaaaagcagg  cgatgcagtc  gaaaactttt  ttaacaacca  aacgcaaaac  1140
63  gcccgcatcg  agttgcgcca  ccaacccata  ggccgtctga  aaggcagctg  gggcgtgcaa  1200
64  tatttgggac  aaaaatccag  tgctttatct  gccacatccg  aagcgggtcaa  acaaccgatg  1260
65  ctgcttgaca  ataaagtgca  acattacagc  tttttcgggtg  tagaacaggc  aaactgggac  1320
66  aacttcacgc  ttgaaggcgg  cgtacgcgtg  gaaaaacaaa  aagcctccat  ccgctacgac  1380
67  aaagcattga  ttgatcgggg  aaactactac  aagcagcccc  tgcccgcacct  cggcgcgcac  1440
68  cgccaaaccg  cccgctcggt  cgcaactttc  ggcaactggg  atttcacgcc  gcaacacaaa  1500
69  ctcagcctga  ccgcctccca  tcaggaacgc  ctgccgtcaa  cgcaagagct  gtacgcacac  1560
70  ggcaaacacg  ttgccacca  cacttttgaa  gtcggcaaca  aacacctgaa  caaagagcgt  1620
71  tccaacaaca  tcgaactcgc  gttgggtac  gaaggcgacc  gctggcaata  caatctggca  1680
72  ctctaccgca  accgcttcgg  caactacatt  tacgcccata  ccttaaacga  cggacgcggc  1740
73  cccaaatcca  tcgaagacga  cagcgaaatg  aagctcgtgc  gctacaacca  atccggtgcg  1800
74  gacttctacg  gcgcggaagg  cgaaatctac  ttcaaaccga  caccgcgcta  ccgcatcggc  1860
75  gtttcggcg  actatgtacg  aggcggtctg  aaaaacctgc  cgtccctacc  cggcagggaa  1920
76  gatgcctacg  gcaaccgtcc  ttcatcgcg  caggacgacc  aaaacgcccc  tcgcgttccg  1980
77  gctgcgcgcc  tcggcttcca  cctgaaagcc  tcgctgaccg  accgcacoga  tgccaatttg  2040
78  gactactacc  gcgtgtttgc  ccaaaacaaa  ctgcgccgct  acgaaacgcg  cacgcccgga  2100
79  caccatatgc  tcaacctcgg  cgcaaactac  cgccgcaata  cgcgctatgg  cgagtggaat  2160
80  tggtagctca  aagccgacaa  cctgctcaac  caatccgttt  acgcccacag  cagcttcctc  2220
81  tctgatacgc  cacaaatggg  ccgcagcttt  accggtggcg  taaacgtgaa  gtttttaa  2277

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83 &lt;210&gt; SEQ ID NO: 2

84 &lt;211&gt; LENGTH: 758

85 &lt;212&gt; TYPE: PRT

86 &lt;213&gt; ORGANISM: Neisseria meningitidis

88 &lt;400&gt; SEQUENCE: 2

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89  Met Ala Gln Thr Thr Leu Lys Pro Ile Val Leu Ser Ile Leu Leu Ile
90  1          5          10          15
91  Asn Thr Pro Leu Leu Ala Gln Ala His Glu Thr Glu Gln Ser Val Gly
92          20          25          30
93  Leu Glu Thr Val Thr Val Val Gly Lys Ser Arg Pro Arg Ala Thr Ser
94          35          40          45
95  Gly Leu Leu His Thr Ser Thr Ala Ser Asp Lys Ile Ile Ser Gly Asp
96          50          55          60
97  Thr Leu Arg Gln Lys Ala Val Asn Leu Gly Asp Ala Leu Asp Gly Val
98  65          70          75          80
99  Pro Gly Ile His Ala Ser Gln Tyr Gly Gly Gly Ala Ser Ala Pro Val
100          85          90          95
101  Ile Arg Gly Gln Thr Gly Arg Arg Ile Lys Val Leu Asn His His Gly
102          100          105          110
103  Glu Thr Gly Asp Met Ala Asp Phe Ser Pro Asp His Ala Ile Met Val
104          115          120          125
105  Asp Thr Ala Leu Ser Gln Gln Val Glu Ile Leu Arg Gly Pro Val Thr
106          130          135          140
107  Leu Leu Tyr Ser Ser Gly Asn Val Ala Gly Leu Val Asp Val Ala Asp
108  145          150          155          160
109  Gly Lys Ile Pro Glu Lys Met Pro Glu Asn Gly Val Ser Gly Glu Leu
110          165          170          175
111  Gly Leu Arg Leu Ser Ser Gly Asn Leu Glu Lys Leu Thr Ser Gly Gly

```

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112          180          185          190
113 Ile Asn Ile Gly Leu Gly Lys Asn Phe Val Leu His Thr Glu Gly Leu
114          195          200          205
115 Tyr Arg Lys Ser Gly Asp Tyr Ala Val Pro Arg Tyr Arg Asn Leu Lys
116          210          215          220
117 Arg Leu Pro Asp Ser Pro Arg Arg Phe Ala Asn Gly Gln His Arg Ala
118 225          230          235          240
119 Val Leu Gly Trp Arg Lys Arg Phe Tyr Arg Arg Thr Tyr Ser Asp Arg
120          245          250          255
121 Arg Asp Gln Tyr Gly Leu Pro Ala His Ser His Glu Tyr Asp Asp Cys
122          260          265          270
123 His Ala Asp Ile Ile Trp Gln Lys Ser Leu Ile Asn Lys Arg Tyr Leu
124          275          280          285
125 Gln Leu Tyr Pro His Leu Leu Thr Glu Glu Asp Val Asp Tyr Asp Asn
126          290          295          300
127 Pro Gly Leu Ser Cys Gly Phe His Asp Asp Asp Ala His Ala His
128 305          310          315          320
129 Ala His Asn Gly Lys Pro Trp Ile Asp Leu Arg Asn Lys Arg Tyr Glu
130          325          330          335
131 Leu Arg Ala Glu Trp Lys Gln Pro Phe Pro Gly Phe Glu Ala Leu Arg
132          340          345          350
133 Val His Leu Asn Arg Asn Asp Tyr His His Asp Glu Lys Ala Gly Asp
134          355          360          365
135 Ala Val Glu Asn Phe Phe Asn Asn Gln Thr Gln Asn Ala Arg Ile Glu
136          370          375          380
137 Leu Arg His Gln Pro Ile Gly Arg Leu Lys Gly Ser Trp Gly Val Gln
138 385          390          395          400
139 Tyr Leu Gly Gln Lys Ser Ser Ala Leu Ser Ala Thr Ser Glu Ala Val
140          405          410          415
141 Lys Gln Pro Met Leu Leu Asp Asn Lys Val Gln His Tyr Ser Phe Phe
142          420          425          430
143 Gly Val Glu Gln Ala Asn Trp Asp Asn Phe Thr Leu Glu Gly Gly Val
144          435          440          445
145 Arg Val Glu Lys Gln Lys Ala Ser Ile Arg Tyr Asp Lys Ala Leu Ile
146          450          455          460
147 Asp Arg Glu Asn Tyr Tyr Lys Gln Pro Leu Pro Asp Leu Gly Ala His
148 465          470          475          480
149 Arg Gln Thr Ala Arg Ser Phe Ala Leu Ser Gly Asn Trp Tyr Phe Thr
150          485          490          495
151 Pro Gln His Lys Leu Ser Leu Thr Ala Ser His Gln Glu Arg Leu Pro
152          500          505          510
153 Ser Thr Gln Glu Leu Tyr Ala His Gly Lys His Val Ala Thr Asn Thr
154          515          520          525
155 Phe Glu Val Gly Asn Lys His Leu Asn Lys Glu Arg Ser Asn Asn Ile
156          530          535          540
157 Glu Leu Ala Leu Gly Tyr Glu Gly Asp Arg Trp Gln Tyr Asn Leu Ala
158 545          550          555          560
159 Leu Tyr Arg Asn Arg Phe Gly Asn Tyr Ile Tyr Ala Gln Thr Leu Asn
160          565          570          575

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161 Asp Gly Arg Gly Pro Lys Ser Ile Glu Asp Asp Ser Glu Met Lys Leu
162          580          585          590
163 Val Arg Tyr Asn Gln Ser Gly Ala Asp Phe Tyr Gly Ala Glu Gly Glu
164          595          600          605
165 Ile Tyr Phe Lys Pro Thr Pro Arg Tyr Arg Ile Gly Val Ser Gly Asp
166          610          615          620
167 Tyr Val Arg Gly Arg Leu Lys Asn Leu Pro Ser Leu Pro Gly Arg Glu
168 625          630          635          640
169 Asp Ala Tyr Gly Asn Arg Pro Phe Ile Ala Gln Asp Asp Gln Asn Ala
170          645          650          655
171 Pro Arg Val Pro Ala Ala Arg Leu Gly Phe His Leu Lys Ala Ser Leu
172          660          665          670
173 Thr Asp Arg Ile Asp Ala Asn Leu Asp Tyr Tyr Arg Val Phe Ala Gln
174          675          680          685
175 Asn Lys Leu Ala Arg Tyr Glu Thr Arg Thr Pro Gly His His Met Leu
176          690          695          700
177 Asn Leu Gly Ala Asn Tyr Arg Arg Asn Thr Arg Tyr Gly Glu Trp Asn
178 705          710          715          720
179 Trp Tyr Val Lys Ala Asp Asn Leu Leu Asn Gln Ser Val Tyr Ala His
180          725          730          735
181 Ser Ser Phe Leu Ser Asp Thr Pro Gln Met Gly Arg Ser Phe Thr Gly
182          740          745          750
183 Gly Val Asn Val Lys Phe
184          755

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186 &lt;210&gt; SEQ ID NO: 3

187 &lt;211&gt; LENGTH: 2112

188 &lt;212&gt; TYPE: DNA

189 &lt;213&gt; ORGANISM: Neisseria meningitidis

191 &lt;400&gt; SEQUENCE: 3

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192 atgaaaatat catttcattt agctttatta cccacgctga ttattgcttc cttccctggt      60
193 gctgccgcgc atacgcagga caatggtgaa cattacaccg ccacgctacc taccgtttcc      120
194 gtggtcggac agtcgcagac cagcgtactc aaaggctaca tcaactacga cgaagccgcc      180
195 gttacccgca acggacagct catcaaagaa acgccgcaaa ccacgcatac gctcaatata      240
196 cagaaaaaca aaaattacgg tacgaacgat ttgagttcca tctcgaagg caatgccggc      300
197 atcgacgctg cctacgatat gcgcggcgaa agcattttcc tgcgcggttt tcaagccgat      360
198 gcatccgata tttaccgcga cggcgtgcgc gaaagcggac aagtgcgcgc cagtactgcc      420
199 aacatcgagc gcgtggaaat cctgaaaggc ccgtcttccg tgctttacgg ccgcaccaac      480
200 ggcggcggcg tcatcaacat ggtcagcaaa tacgccaaact tcaaacaaag ccgcaacata      540
201 ggtgcggttt acggttcgtg ggcaaacgcg agcctgaata tggacattaa cgaagtgtct      600
202 aacaaaaacg tcgccatccg tctcaccggc gaagtcgggc gcgccaatte gttccgcagc      660
203 ggcatagaca gcaaaaatgt catggtttca cccagcatta ccgtcaaact cgacaacggc      720
204 ttgaaatgga cggggcaata cacctacgac aatgtggagc gcacgcccga ccgcagtcgc      780
205 accaagtccg tgtacgaccg cttcggactg ccttaccgca tgggggttcgc ccaccggaac      840
206 gattttgtca aagacaagct gcaagtttgg cgttccgacc ttgaatacgc cttcaacgac      900
207 aaatggcggt cccaatggca gctcgcccac cgcaaggcgg cgcaggattt tgatcatttc      960
208 tatgcaggca gcgaaaatgg caacttaata aaacgtaact acgcctggca gcagaccgac      1020
209 aacaaaaacc tgtcgtccaa cttcacgctc aaaggcgact acaccatcgc ccgttttgaa      1080
210 aaccacctga ccgtaggcat ggattacagc cgcgaacacc gcaacccgac attgggtttc      1140
211 agacgcaact ttaccgcctc catcgatcca tacgaccgcg caagcaggcc ggcttcgggc      1200

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212 agattgcagc gtattctggc ccaagaccgg cacaaagccg actcctacgg catcttcgtg 1260
213 caaaacatct tctccgccac gcccgatttg aaattcgtcc tcggcggtcg ttacgacaag 1320
214 tacaccttta attccgaaaa caaactcacc ggcagcagcc gccagtacag cggacactcg 1380
215 ttcagcccca acatcgggtg agtgtggaac atcaatcccg tccacacact ttacgcctcg 1440
216 tataacaaaag cgttcgcgcc ttatggcgga cgcggcggct atttgagcat caacacgtcg 1500
217 tcttccgccc tggtcaacgc cgaccccgag tacacccgcc aatacgaaac cggcgtaaaa 1560
218 agcagttggc tggacgaccg cctcagcacc acattgtccg cctaccaaat cgaacgcttc 1620
219 aatatccgct accgccccga cgagcaaaat gatccctaca cttgggcagt cggcggtaaa 1680
220 caccgttcgc gcggcgtgga attgtccgcc atcgggcaaa tcatccccaa aaaactctat 1740
221 ctgcgcggtt cgttgggcgt gatgcaggcg aaagtcggtg aagacaaaaa aaatcccgcac 1800
222 cgagtgggca tccatttgaa taataccagc aacgttaccg gcaacctgtt tttccggtat 1860
223 acaccgaccg aaaacctcta cggcgaaatc ggcgtaaccg gtacaggcaa acgctacggt 1920
224 tacaactcaa gaaataaaga agtgactacg cttccaggct ttgcccagat tgatgccatg 1980
225 ctcggctgga accataaaaa tggttaacgtt acctttgccg cagccaatct gttcaatcaa 2040
226 aaatattggc gttcggactc tatgccgggt aatccgcgcg gctatactgc ccgggtaaat 2100
227 taccgtttct ga 2112

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229 &lt;210&gt; SEQ ID NO: 4

230 &lt;211&gt; LENGTH: 703

231 &lt;212&gt; TYPE: PRT

232 &lt;213&gt; ORGANISM: Neisseria meningitidis

234 &lt;400&gt; SEQUENCE: 4

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235 Met Lys Ile Ser Phe His Leu Ala Leu Leu Pro Thr Leu Ile Ile Ala
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238 20 25 30
239 Thr Ala Thr Leu Pro Thr Val Ser Val Val Gly Gln Ser Asp Thr Ser
240 35 40 45
241 Val Leu Lys Gly Tyr Ile Asn Tyr Asp Glu Ala Ala Val Thr Arg Asn
242 50 55 60
243 Gly Gln Leu Ile Lys Glu Thr Pro Gln Thr Ile Asp Thr Leu Asn Ile
244 65 70 75 80
245 Gln Lys Asn Lys Asn Tyr Gly Thr Asn Asp Leu Ser Ser Ile Leu Glu
246 85 90 95
247 Gly Asn Ala Gly Ile Asp Ala Ala Tyr Asp Met Arg Gly Glu Ser Ile
248 100 105 110
249 Phe Leu Arg Gly Phe Gln Ala Asp Ala Ser Asp Ile Tyr Arg Asp Gly
250 115 120 125
251 Val Arg Glu Ser Gly Gln Val Arg Arg Ser Thr Ala Asn Ile Glu Arg
252 130 135 140
253 Val Glu Ile Leu Lys Gly Pro Ser Ser Val Leu Tyr Gly Arg Thr Asn
254 145 150 155 160
255 Gly Gly Gly Val Ile Asn Met Val Ser Lys Tyr Ala Asn Phe Lys Gln
256 165 170 175
257 Ser Arg Asn Ile Gly Ala Val Tyr Gly Ser Trp Ala Asn Arg Ser Leu
258 180 185 190
259 Asn Met Asp Ile Asn Glu Val Leu Asn Lys Asn Val Ala Ile Arg Leu
260 195 200 205
261 Thr Gly Glu Val Gly Arg Ala Asn Ser Phe Arg Ser Gly Ile Asp Ser
262 210 215 220

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**VERIFICATION SUMMARY**

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date